D   AAA41767 standard; cDNA; 374 BP.
X
C   AAA41767;
X   XP-002397256
T   21-AUG-2000   (first entry)
X
E   Human secreted expressed sequence tag SEQ ID NO:507.
X
W   Human; mouse; xenopus; rat; secreted expressed sequence tag; sEST;
W   expressed sequence tag; EST; probe; chemotactic; proliferative;
W   immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;
W   thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;
W   antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian;
W   antiulcer; osteopathic; neuroprotective; nootropic; antipsoriatic;
W   cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine;
W   autoimmune disorder; multiple sclerosis; allergic condition;
W   insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
W   lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
W   central nervous system disorder; Alzheimer's disease; stroke;
V   Parkinson's disease; Huntington's disease; coagulation disorder;
V   haemophilia; thrombosis; inflammatory disorder; Crohn's disease; tumour;
V   infection; depression; psoriasis; ss.
<
;   omo sapiens.
<
I   WO200021990-A1
C
)   20-APR-2000.

     15-OCT-1999;   99WO-US024205.

     15-OCT-1998;   98US-0104435P.

     (GEMY) GENETICS INST INC.

     Jacobs K, Mccoy JM, Lavallie ER, Collins-Racie LA, Evans C;
     Merberg D, Treacy M;

     WPI; 2000-317937/27.

     Isolated polynucleotides, and encoded proteins, comprising secreted
     expressed sequence tags (sESTs), useful for treating various disorders
     such as autoimmune, infectious, and central nervous system disorders.

     Claim 1; Page 277; 618pp; English.

     AAA41261 to AAA43419 represent specifically claimed secreted expressed
     sequence tags (sESTs), isolated from human, mouse, xenopus and rat tissue
     sources. The sESTs can have a range of activities depending on the
     tissues they were isolated from. The activities include: chemotactic;
     proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic;
     haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial;
     antifungal; antiviral; antidiabetic; antiasthmatic; vulnerary; antiulcer;
     osteopathic; neuroprotective; nootropic; antiparkinsonian; antipsoriatic;
     cerebroprotective; anticonvulsant; and antidepressant. The sESTs can be
     used for gene therapy and in vaccines. The sESTs are useful as probes for
     the identification and isolation of full-length cDNAs and genomic DNA
     molecules which correspond to the sESTs. Proteins encoded by the sESTs
     are useful in assays for determining biological activity and raising
     antibodies. They may be useful for treatment of autoimmune disorders
     (multiple sclerosis, insulin dependent diabetes), allergic conditions
     (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
     osteoporosis, osteoarthritis, central nervous system disorders
     (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation
     disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
     disease), tumours, bacterial, fungal or viral infections, depression and
     psoriasis. AAA43420 to AAA43425 represent linker variants which are given
     in the exemplification of the present invention

```
XX
SQ    Sequence 374 BP; 103 A; 85 C; 93 G; 93 T; 0 U; 0 Other;
      gaattcgcgg ccgcgtcgac gtactctaaa gttagaatct cctgatcttt cacgagatgc          60
      tggactggag attggcaagt gcacatttca tcctggctgt gacactgaca ctgtggagct         120
      caggaaaagt cctctcagta gatgtaacaa caacagaggc ctttgattct ggagtcatag         180
      atgtgcagtc aacacccaca gtcagggaag agaaatcagc cactgacctg acagcaaaac         240
      tcttgcttct tgatgaattg gtgtccctag aaaatgatgt gattgagaca aagaagaaaa         300
      ggagtttctc tggttttggg tctccccttg acagactctc agctggctct gtagatcaca         360
      aaggtccgct cgag                                                           374
//
```

Blast 2 Sequences results

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure
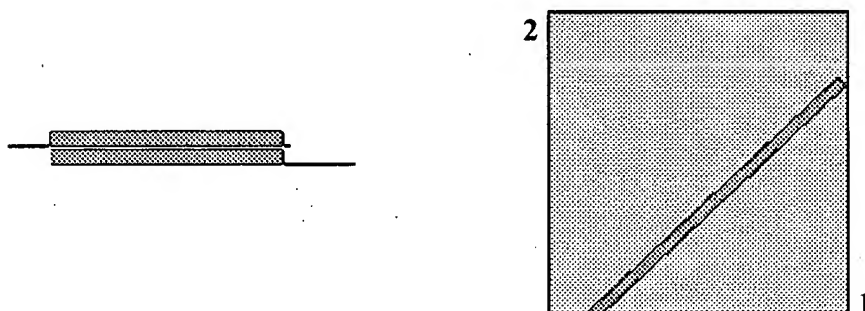
BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.16 [Mar-25-2007]

Match: 1   Mismatch: -2   gap open: 5   gap extension: 2

x_dropoff: 0   expect: 10.000C wordsize: 11   Filter ☐ View option Standard

Masking character option X for protein, n for nucleotide   Masking color option Black

☐ Show CDS translation   [Align]

Sequence 1: lcl|seq_1
Length = 373 (1 .. 373)

Sequence 2: lcl|seq_2
Length = 402 (1 .. 402)

NOTE:Bitscore and expect value are calculated based on the size of the nr database.

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence.


```
 Score =  594 bits (309),  Expect = 6e-167
 Identities = 309/309 (100%), Gaps = 0/309 (0%)
 Strand=Plus/Plus
```

SEQ ID No: 57 of WO2002/1990

```
Query  57   ATGCTGGACTGGAGATTGGCAAGTGCACATTTCATCCTGGCTGTGACACTGACACTGTGG  116
            ||I.|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    ATGCTGGACTGGAGATTGGCAAGTGCACATTTCATCCTGGCTGTGACACTGACACTGTGG  60
```

Applicants SEQ ID No: 1

```
Query  117  AGCTCAGGAAAAGTCCTCTCAGTAGATGTAACAACAACAGAGGCCTTTGATTCTGGAGTC  176
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   AGCTCAGGAAAAGTCCTCTCAGTAGATGTAACAACAACAGAGGCCTTTGATTCTGGAGTC  120

Query  177  ATAGATGTGCAGTCAACACCCACAGTCAGGGAAGAGAAATCAGCCACTGACCTGACAGCA  236
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Sbjct   121   ATAGATGTGCAGTCAACACCCACAGTCAGGGAAGAGAAATCAGCCACTGACCTGACAGCA   180

Query   237   AAACTCTTGCTTCTTGATGAATTGGTGTCCCTAGAAAATGATGTGATTGAGACAAAGAAG   296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   181   AAACTCTTGCTTCTTGATGAATTGGTGTCCCTAGAAAATGATGTGATTGAGACAAAGAAG   240

Query   297   AAAAGGAGTTTCTCTGGTTTTGGGTCTCCCCTTGACAGACTCTCAGCTGGCTCTGTAGAT   356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   241   AAAAGGAGTTTCTCTGGTTTTGGGTCTCCCCTTGACAGACTCTCAGCTGGCTCTGTAGAT   300

Query   357   CACAAAGGT   365
              |||||||||
Sbjct   301   CACAAAGGT   309
```

CPU time: 0.02 user secs.   0.02 sys. secs   0.04 total secs.